In the claims:

Claims 1-26 **(canceled)**

27. **(currently amended)** A method for identifying drug candidates comprising:

(a) transforming a <u>first set of</u> host cell<u>s</u> with ~~the~~ <u>a first set of</u> plasmid<u>s,</u> ~~of claim 1~~ <u>each plasmid comprising a first mutant rRNA gene and a first selectable marker gene;</u>

<u>wherein said mutant rRNA gene comprises at least one mutation and a first mutant Anti-Shine-Dalgarno sequence; and said first selectable marker gene comprises a first mutant Shine-Dalgarno sequence; and</u>

<u>wherein said first mutant Anti-Shine-Dalgarno sequence and said first mutant Shine-Dalgarno sequence are a mutually compatible pair;</u>

<u>thereby forming a first set of transformed host cells;</u>

(b) isolating <u>from the first set of transformed host cells those host</u> cells [[via]] <u>which express</u> the selectable marker <u>gene product;</u>

(c) ~~identifying and~~ sequencing the <u>first mutant</u> rRNA <u>gene</u> from <u>each host cell isolated in</u> step (b) to identify ~~the~~ regions of interest<u>, wherein the regions of interest comprise sequences of one or more nucleic acids which are conserved in each first mutant rRNA gene sequenced;</u>

~~(d) selecting regions of interest from step (c);~~

~~(e)~~ <u>(d)</u> generating a second plurality of mutant rRNA genes wherein ~~mutating~~ the regions of interest from step (c) <u>are mutated; and each rRNA gene further comprises a second mutant Anti-Shine-Dalgarno sequence;</u>

~~(f)~~ <u>(e)</u> inserting the <u>second plurality of mutant rRNA</u> genes <u>comprising the</u> mutated regions of interest from step ~~(e)~~ <u>(d)</u> into <u>a second plurality of</u> plasmid<u>s; wherein said plasmids further comprise</u> ~~comprising an rRNA gene having a mutant Anti-Shine-Dalgarno sequence and~~ a <u>second</u> genetically engineered gene which encodes a <u>second</u> selectable marker having a <u>second</u> mutant Shine-Dalgarno sequence, wherein the <u>second</u> mutant Anti-Shine-Dalgarno and the <u>second</u> mutant Shine-Dalgarno sequence are a mutually compatible pair;

(g) (f) transforming [[a]] a second set of host cells with the plasmids from step (f) (e), thereby forming a second set of transformed host cells;

(h) (g) isolating from the second set of transformed host cells from step (g) (f) [[via]] those host cells which express the selectable marker gene product;

(i) (h) identifying sequencing the rRNA gene from each host cell isolated in step (h) (g) to identify the mutated regions of interest functional mutant ribosomes;

(j) (i) screening drug candidates against the mutated regions of interest functional mutant ribosomes from step (i) (h) and the wildtype rRNA;

(k) (j) identifying the drug candidates from step (j) (i) that bound bind to the mutated regions of interest functional mutant ribosomes from step (i) (h) and the wildtype rRNA;

(l) (k) screening the drug candidates from step (k) (j) against a human rRNA; and

(m) (l) identifying the drug candidates from step (l) (k) that do not bind to the human rRNA, thereby identifying drug candidates.

28.   (currently amended) A method for identifying drug candidates comprising:

(a)   transforming a first set of host cells with the a first set of plasmids, of claim 1 each plasmid comprising a first mutant *E. coli* 16S rRNA gene and a first selectable marker gene;

wherein said mutant *E. coli* 16S rRNA gene comprises at least one mutation and a first mutant Anti-Shine-Dalgarno sequence; and said first selectable marker gene comprises a first mutant Shine-Dalgarno sequence; and

wherein said first mutant Anti-Shine-Dalgarno sequence and said first mutant Shine-Dalgarno sequence are a mutually compatible pair;

thereby forming a first set of transformed host cells;

(b)   isolating from the first set of transformed host cells those host cells [[via]] which express the selectable marker gene product;

(c)   identifying and sequencing the first mutant rRNA gene from each host cell isolated in step (b) to identify the regions of interest, wherein the regions of

interest comprise sequences of one or more nucleic acids which are conserved in each first mutant rRNA gene sequenced;

(d)   ~~selecting regions of interest from step (c);~~

~~(e)~~ (d)   generating a second plurality of mutant rRNA genes wherein ~~mutating~~ the regions of interest from step (c) are mutated; and each rRNA gene further comprises a second mutant Anti-Shine-Dalgarno sequence;

~~(f)~~ (e)   inserting the second plurality of mutant *E. coli* 16S rRNA genes comprising the mutated regions of interest from step ~~(e)~~ (d) into a second plurality of plasmids; wherein said plasmids further comprise ~~comprising an *E. coli* 16S rRNA gene having a mutant Anti-Shine-Dalgarno sequence and~~ a genetically engineered gene which encodes ~~GFP~~ green fluorescent protein having a second mutant Shine-Dalgarno sequence, wherein the second mutant Anti-Shine-Dalgarno and the second mutant Shine-Dalgarno sequence are a mutually compatible pair;

~~(g)~~ (f)   transforming [[a]] a second set of host cells with the plasmids from step ~~(f)~~ (e), thereby forming a second set of transformed host cells;

~~(h)~~ (g)   isolating from the second set of transformed host cells from step ~~(g)~~ (f) [[via]] those host cells which express ~~the selectable marker~~ a genetically engineered gene which encodes green fluorescent protien;

~~(i)~~ (h)   ~~identifying~~ sequencing the rRNA genes from each host cell isolated in step ~~(h)~~ (g) to identify the mutated regions of interest ~~functional mutant ribosomes~~;

~~(j)~~ (i)   screening drug candidates against the the mutated regions of interest ~~functional mutant ribosomes~~ from step ~~(i)~~ (h) and the wildtype 16S rRNA;

~~(k)~~ (j)   identifying the drug candidates from step ~~(j)~~ (i) that ~~bound~~ bind to the mutated regions of interest ~~functional mutant ribosomes~~ from step ~~(i)~~ (h) and the wildtype 16S rRNA;

~~(l)~~ (k)   screening the drug candidates from step ~~(k)~~ (j) against a human 16S rRNA; and

~~(m)~~ (l)   identifying the drug candidates from step ~~(l)~~ (k) that do not bind to the human 16S rRNA, thereby identifying drug candidates.

Claims 29-36 **(canceled)**

37.   (new) The method of claim 27, wherein said first mutant rRNA gene is selected from the rRNA genes of *Escherichia coli, Mycobacterium tuberculosis, Pseudomonas aeruginosa, Salmonella typhi, Yersenia pestis, Staphylococcus aureus, Streptococcus pyogenes, Enterococcus faecalis, Chlamydia trachomatis, Saccharomyces cerevesiae, Candida albicans,* and trypanosomes.

38.   (new) The method of claim 27, wherein said first mutant rRNA gene is a 16S rRNA gene.

39.   (new) The method of claim 27, wherein said first mutant Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

40.   (new) The method of claim 27, wherein said first mutant Anti-Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

41.   (new) The method of claim 27, wherein said second mutant Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

42.   (new) The method of claim 27, wherein said second mutant Anti-Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

43.   (new) The method of claim 27, wherein said first selectable marker is selected from the group consisting of chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), or both.

44.   (new) The method of claim 27, wherein said second selectable marker is selected from the group consisting of chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), or both.

45.   (new) The method of claim 28, wherein said first mutant Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

46.   (new) The method of claim 28, wherein said first mutant Anti-Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

47.   (new) The method of claim 28, wherein said second mutant Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

48.   (new) The method of claim 28, wherein said second mutant Anti-Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

49.   (new) The method of claim 28, wherein said first selectable marker is selected from the group consisting of chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), or both.